

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph bridging pages 11 and 12 of the specification with the following rewritten paragraph:

The phrase, "sequence identification," in the present invention means the identification and homology between two DNA sequences and between two protein sequences. The sequence identification may be determined by comparing two sequences aligned in the optimum states in a region of the sequences of the comparison objects. The DNA or proteins, the comparison objects, may have addition or deletion (e.g. gap and the like) in the optimum alignment of two sequences. Regarding such sequence identification, computation may be performed using, for example, Vector NT1 by producing alignment by utilizing Clusta 1W algorithm [Nucleic Acid Res., 22(22): 4673-4680 (1994)]. Incidentally, the sequence identification may be measured by a sequence analysis soft, practically Vector NT1, GENETYX-MAC and anaolysis tools provided in public database. ~~The aforementioned public database may be, in general, accessible in, for example, home address; http://www.ddbj.nig.ac.jp.~~

Please replace the last full paragraph on page 13 of the specification with the following rewritten paragraph:

Next, mRNA is prepared from the total RNA. For example, the preparation may be carried out by a method utilizing the hybridization of oligo-dT chains bonded with ellulose or latex and poly-A chains of mRNA. For the operation, for example, commercialized kits such as mRNA Purification Kit (produced by Amersham Pharmacia Co.), ~~Oligotex TM dt30 (super)~~

OLIGOTEX™ dt30 super (Oligo (dT) latex beads) (produced by Takara Shuzo Co. Ltd.), and the like may be employed.

Please replace the paragraph bridging pages 14 and 15 of the specification with the following rewritten paragraph:

In the case of employing PCR, DNA usable as a primer set is those planned and synthesized based on the nucleotide sequences of about 20 bp to 40 bp, for example, the nucleotide sequences selected respectively from 5'-non-translation regions and 3'-non-translated regions of the nucleotide sequence represented by SEQ ID No: 1, 3, or 5. Examples of the primer set are sets of DNA of nucleotide sequence represented by SED ID No: 9 and DNA of nucleotide sequence represented by SEQ ID No: 10. The PCR solution to be used may be prepared by adding reaction solutions instructed by the kit to cDNA 250 ng. The conditions of the PCR may properly be changed depending on the primer set to be used and, for example, concrete conditions include as follows: keeping at 94°C for 2 minutes, at about 8°C for 3 minutes, and further repeating 40 cycles each of which comprises steps of keeping at 94°C for 30 seconds, at 55°C for 30 seconds, and at 72°C for 4 minutes; and repeating 5-10 cycles each of which comprises steps of keeping at 94°C for 5 seconds and at 72°C for 4 minutes and further repeating about 20 to 40 cycles each of which comprises steps of keeping at 94°C for 5 seconds and at 70°C for 4 minutes. For the operation, the following commercialized kits may be, for example, employed: TakaraHERCULASE Herculase™ (produced by StratageneTakara Shuzo Co., Ltd.), DNA polymerase contained in Advantage cDNA PCR kit (Clontech Co.), TAKARA

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Ex Taq (Takara Shuzo Co. Ltd.), ~~PLATINUM™ PLATINUM™ PCR SUPER (thermostable DNA polymerase in a PCR reaction mix) Mix~~ (Lifetech Oriental Co.), and the like.

Please replace the second full paragraph on page 16 of the specification with the following rewritten paragraph:

In order to obtain DNA coding the cytokinin receptor of Arabidopsis, PCR is carried out employing TAKARA LA ~~TAQTM (thermostable polymerase)~~ (Takara Shuzo Co., Ltd.) and using a solution containing cDNA library phage of Arbidopsis (about 1,000,000 pfu) as a template and DNA having the nucleotide sequence represented by SEQ ID No: 11 and DNA having the nucleotide sequence represented by SEQ ID No: 12 as a primer set to amplify and obtain DNA to be a probe. The PCR solution to be used may be prepared by adding the reaction solutions instructed by the kit to 250 ng of cDNA library.

Please replace the first full paragraph on page 22 of the specification with the following rewritten paragraph:

Such cytokinin receptor of partially transmembrane regions-deleted type are cytokinin receptors whose transmembrane region structure may be assumed by employing structure assumption software available in http://www.ch.embnet.org/software/TMPRED_form.html and whose transmembrane regions are partially deleted, for example, in 1 to 2 sites and are less in number than the number of the transmembrane regions of the natural type cytokinin receptors (i.e. natural form).

Please replace the paragraph bridging pages 38 and 39 with the following rewritten paragraph:

Seeds of *Arabidopsis thaliana* ecotype Wassilewskija were sterilized with 70% of ethyl alcohol for 1 minute and further sterilized with 1.5% of sodium hypochlorite for 10 minutes. The resulting seeds were well washed with sterilized water and then cultured for 2 weeks in GM culture medium [4.3 g Murashige and Skoog's basal salt mixture, 1% sucrose, 10 ml of 5% MES-KOH (pH 5.7), 0.3% PHYTAGEL™ Phytigel™ gellan gum (SIGMA)] to obtain 5g of the plant. After the plant was frozen in liquified~~liquefied~~ nitrogen and physically milled with a mortar and a pestle. The resulting milled product was mixed with a mixed solution of 10 ml of an extraction buffer [200 mM Tris-HCL (pH 8.5), 100 mM NaCl, 10 mM EDTA, 0.5% SDS, 14 mM β-mercaptoethanol] and 10 g of phenol. After being mixed by a Voltex mixter, the resulting mixture was mixed further with 10 ml of chloroform and vigorously stirred and subjected to centrifugal separation at 10,000 rotation for 20 minutes. The recovered aqueous layer was mixed with LiCl in the concentration to be 2M of the final concentration, left still at -80°C for 3 hours, thawed and subjected to centrifugal separation at 10,000 rotation for 20 minutes to recover a precipitate. The recovered precipitate was dissolved in 2 ml of TE [10 mM Tris-HCl (pH 8.0), 1mM EDTA] and then further mixed with 0.2 ml of 3 M sodium acetate (pH 5.2) and 5 ml ethanol and subjected to centrifugal separation to recover RNA as a precipitate. Further, the precipitate (RNA) was subjected to treatment with Oligotex™ dT30super OLIGOTEX™ dt30super (oligo d(T) latex beads) (Nippon Rosh Co.) to extract RNA integrated with polyA.

Please replace the paragraph bridging pages 42 and 43 of the specification with the following rewritten paragraph:

Seeds of *Arabidopsis thaliana* ecotype Wassilewskija were sterilized with 70% of ethyl alcohol for 1 minute and further sterilized with 1.5% of sodium hypochlorite for 10 minutes. The resulting seeds were well washed with sterilized water and then cultured for 2 weeks in GM culture medium [4.3 g Murashige and Skoog's basal salt mixture, 1% sucrose, 10 ml pf 5% MES-KOH (pH 5.7), 0.3 Phytigel™ PHYTAGEL™ (gellan gum) (SIGMA)] to obtain 5 g of the plant. After the plant was frozen in liquefied nitrogen and physically milled with a mortar and pestle. The resulting milled product was mixed with a mixed solution of 10 ml of an extraction buffer [200 mM Tris-HCl (pH 8.5), 100 mM NaCl, 10 mM EDTA, 0.5% SDS, 14 mM β-mercaptoethanol] and 10 g of phenol. After being mixed with a Voltex mixer, the resulting mixture was mixed further with 10 ml of chloroform and vigorously stirred and subjected to centrifugal separation at 10,000 rotation for 20 minutes. The recovered aqueous layer was mixed with LiCl in the concentration to be 2M of the final concentration, left still at -80°C for 3 hours, thawed and subjected to centrifugal separation at 10,000 rotation for 20 minutes to recover a precipitate. The recovered precipitate was dissolved in 2 ml of TE [10 mM Tris-HCl (pH 8.0), 1 mM EDTA] and then further with 0.2 ml of 3 M sodium acetate (pH 5.2) and 5 ml ethanol and subjected to centrifugal separation to recover RNA as a precipitate. Further, 40 µg of the precipitate (RNA) was mixed with 30 unit of FPLC pure™ DnaseI (RNase free-DNase I) (Amersham-Pharmacia) and 60 unit of Superace (Ambion) to remove mixed genome DNA and

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the resulting RNA was subjected to the phenol/chloroform treatment and ethanol treatment to purify the RNA. Next, using the purified RNA as a template and oligo (dT) 12-18 (Amersham-Pharmacia) as a primer, RT-PCR was carried out. The RT-PCR was carried out employing Superscript II (GIBCO BRL Co.) at 42°C for 40 minutes. Incidentally the PT-PCR solution was prepared according to the method described in instruction of the Superscript II.